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RAW SEQUENCE LISTING

DATE: 02/10/2004

PATENT APPLICATION: US/10/763,992

TIME: 10:10:47

Input Set : N:\Crf3\RULE60\10763992.RAW.txt

Output Set: N:\CRF4\02102004\J763992.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:
4 (i) APPLICANT: COHEN, Maurice
5 FRIEDMAN, Paula N.
6 GORDON, Julian
7 HODGES, Steven C.
8 KLASS, Michael R.
9 KRATOCHVIL, Jon D.
10 ROBERTS-RAPP, Lisa
11 RUSSELL, John C.
12 STROUPE, Steven D.
13 (ii) TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
14 FOR DETECTING DISEASES OF THE PROSTATE
15 (iii) NUMBER OF SEQUENCES: 35
16 (iv) CORRESPONDENCE ADDRESS:
17 (A) ADDRESSEE: Abbott Laboratories
18 (B) STREET: 100 Abbott Park Road
19 (C) CITY: Abbott Park
20 (D) STATE: IL
21 (E) COUNTRY: USA
22 (F) ZIP: 60064-3500
23 (v) COMPUTER READABLE FORM:
24 (A) MEDIUM TYPE: Diskette
25 (B) COMPUTER: IBM Compatible
26 (C) OPERATING SYSTEM: DOS
27 (D) SOFTWARE: FastSEQ for Windows Version 2.0
28 (vi) CURRENT APPLICATION DATA:
C--> 29 (A) APPLICATION NUMBER: US/10/763,992
C--> 30 (B) FILING DATE: 22-Jan-2004
31 (C) CLASSIFICATION:
35 (vii) PRIOR APPLICATION DATA:
33 (A) APPLICATION NUMBER: US/09/418,887
34 (B) FILING DATE: 15-OCT-1999
36 (A) APPLICATION NUMBER: US/08/946,869
37 (B) FILING DATE: 08-Oct-1997
38 (viii) ATTORNEY/AGENT INFORMATION:
39 (A) NAME: Becker, Cheryl L.
40 (B) REGISTRATION NUMBER: 35,441
41 (C) REFERENCE/DOCKET NUMBER: 5697.US.P1
42 (ix) TELECOMMUNICATION INFORMATION:
43 (A) TELEPHONE: 847/935-1729
44 (B) TELEFAX: 847/938-2623
45 (C) TELEX:

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46 (2) INFORMATION FOR SEQ ID NO: 1:

47 (i) SEQUENCE CHARACTERISTICS:

48 (A) LENGTH: 367 base pairs

49 (B) TYPE: nucleic acid

50 (C) STRANDEDNESS: single

51 (D) TOPOLOGY: linear

52 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

| | | |
|----|---|-----|
| 53 | TGCGCNGGAG CCTGAGCGGA GGGTGTGCGC AGCCTCGCCA GCGGGGGCCC GGGGCTGNCG | 60 |
| 54 | CATTGCCTCA CTGAGCCAGC GCCTGCCTNC TACCTCGCCG ACAGCTGGAA CCAGTGCGAC | 120 |
| 55 | CTAGTGCTC TCACCTGCTT CCTCCTGGGC GTGGGCTGCC GGCTGACCCC GGGTTTGAC | 180 |
| 56 | CACCTGGGCC GCACTGTCCT CTGCATCGAC TTCATGGTTT TCACGGTGCG GCTGCTTCAC | 240 |
| 57 | ATCTTCACGG TCAACAAACA GCTGGGGCCC AAGATCGTCA TCGTGAGCAA GATGATGAAG | 300 |
| 58 | GACGTGTTCT TCTTCCTCTT CTTCTCGGC GTGTGGCTGG TAGCTATGGG TTGGGCCACG | 360 |
| 59 | GAGGGGT | 367 |

61 (2) INFORMATION FOR SEQ ID NO: 2:

62 (i) SEQUENCE CHARACTERISTICS:

63 (A) LENGTH: 214 base pairs

64 (B) TYPE: nucleic acid

65 (C) STRANDEDNESS: single

66 (D) TOPOLOGY: linear

67 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

| | | |
|----|---|-----|
| 68 | CAAACAGCTG GGGCCCAAGA TCGTCATCGT GAGCAAGATG ATGAAGGACG TGTTCTTCTT | 60 |
| 69 | CCTCTTCTTC CTCGGCGTGT GGCTGGTAGC CTATGGCGTG GCCACGGAGG GGCTCCTGAG | 120 |
| 70 | GCCACGGGAC AGTGACTTCC CAAGTATCCT GCGCCGCGTC TTCTACCGTC CCTACCTGCA | 180 |
| 71 | GATCTTCGGG CAGATTCCCC AGGAGGACAT GGAC | 214 |

73 (2) INFORMATION FOR SEQ ID NO: 3:

74 (i) SEQUENCE CHARACTERISTICS:

75 (A) LENGTH: 205 base pairs

76 (B) TYPE: nucleic acid

77 (C) STRANDEDNESS: single

78 (D) TOPOLOGY: linear

79 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

| | | |
|----|---|-----|
| 80 | CGTGTGGCTG GTAGCCTATG GCGTGGCCAC GGAGGGGCTC CTGAGGCCAC GGGACAGTGA | 60 |
| 81 | CTTCCCAAGT ATCCTGCGCC GCGTCTTCTA CCGTCCCTAC CTGCAGATCT TCGGGCAGAT | 120 |
| 82 | TCCCCAGGAG GACATGGACG TGGCCCTCAT GGAGCACAGC AACTGCTCGT CGGAGCCCGG | 180 |
| 83 | CTTCTGGGCA CACCCTCCTG GGGCC | 205 |

85 (2) INFORMATION FOR SEQ ID NO: 4:

86 (i) SEQUENCE CHARACTERISTICS:

87 (A) LENGTH: 256 base pairs

88 (B) TYPE: nucleic acid

89 (C) STRANDEDNESS: single

90 (D) TOPOLOGY: linear

91 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

| | | |
|----|---|-----|
| 92 | CGGGCAGATT CCCCAGGAGG ACATGGACGT GGCCCTCATG GAGCACAGCA ACTGCTCGTC | 60 |
| 93 | GGAGCCCGGC TTCTGGGCAC ACCCTCCTGG GGCCAGGCG GGCACCTGCG TCTCCCAGTA | 120 |
| 94 | TGCCAACTGG CTGGTGGTGC TGCTCCTCGT CATCTTCCTG CTCGTGGCCA ACATCCTGCT | 180 |
| 95 | GGTCAACTTG CTCATTGCCA TGTTCAAGTA CACATTCCGC AAAGTACAGG GCAACAGCGA | 240 |
| 96 | TCTCTACTGG AAGGCG | 256 |

98 (2) INFORMATION FOR SEQ ID NO: 5:

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99      (i) SEQUENCE CHARACTERISTICS:
100      (A) LENGTH: 246 base pairs
101      (B) TYPE: nucleic acid
102      (C) STRANDEDNESS: single
103      (D) TOPOLOGY: linear
104      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
105      GCGATCTCTA CTGGAAGGCG CAGGTTACCG CCTCATCCGG GAATTCCACT CTCGGCCCCG      60
106      GCTGGCCCCG CCCTTTATCG TCATCTCCCA CTTGCGCCTC CTGCTCAGGC AATTGTGCAG      120
107      GCGACCCCGG AGCCCCCAGC CGTCCTCCCC GGCCCTCGAG CATTTCGGGG TTTACCTTTC      180
108      TAAGGAAGCC GAGCGGAAGC TGCTAACGTG GGAATCGGTG CATAAGGAGA ACTTTCTGCT      240
109      GGCACG                                     246
111 (2) INFORMATION FOR SEQ ID NO: 6:
112      (i) SEQUENCE CHARACTERISTICS:
113      (A) LENGTH: 277 base pairs
114      (B) TYPE: nucleic acid
115      (C) STRANDEDNESS: single
116      (D) TOPOLOGY: linear
117      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
118      GTGCATAAGG AGAACTTTCT GCTGGCACGC GCTAGGGACA AGCGGGAGAG CGACTCCGAG      60
119      CGTCTGAAGC GCACGTCCCA GAAGGTGGAC TTGGCACTGA AACAGCTGGG ACACATCCGC      120
120      GAGTACGAAC AGCGCCTGAA AGTGCTGGAG CGGGAGGTCC AGCAGTGTAG CCGCGTCCTG      180
121      GGGTGGGTGG CCGAGGCCCT GAGCCGCTCT GCCTTGCTGC CCCCAGGTGG GCCGCCACCC      240
122      CCTGACCTGC CTGGGTCCAA AGACTGAGCC CTGCTGG                                     277
124 (2) INFORMATION FOR SEQ ID NO: 7:
125      (i) SEQUENCE CHARACTERISTICS:
126      (A) LENGTH: 251 base pairs
127      (B) TYPE: nucleic acid
128      (C) STRANDEDNESS: single
129      (D) TOPOLOGY: linear
130      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
131      GGGTCCAAAG ACTGANCCCT GCTGGCGGAC TTCAAGGAGA AGCCCCCACA GGGGATTTTG      60
132      CTCCTAGAGT AAGGCTCATC TGGGCCTCGG CCCCCGCACC TGGTGGCCTT GTCCTTGAGG      120
133      TGAGCCCCAT GTCCATCTGG GCCACTGTCA GGACCACCTT TGGGAGTGTC ATCCTTACAA      180
134      ACCACAGCAT GCCCGGCTCC TCCCAGAACC AGTCCCAGCC TGGGAGGATC AAGGCCTGGA      240
135      TCCCGGGCCG T                                     251
137 (2) INFORMATION FOR SEQ ID NO: 8:
138      (i) SEQUENCE CHARACTERISTICS:
139      (A) LENGTH: 223 base pairs
140      (B) TYPE: nucleic acid
141      (C) STRANDEDNESS: single
142      (D) TOPOLOGY: linear
143      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
144      GGCTCATCTG GGCCTCGGCC CCCGCACCTG GTGGCCTTGT CCTTGAGGTG AGCCCCATGT      60
145      CCATCTGGGC CACTGTCAGG ACCACCTTTG GGAGTGTGTC CTTACAAAC CACAGCATGC      120
146      CCGGCTCCTC CCAGAACCAG TCCCAGCCTG GGAGGATCAA GGCCTGGATC CCGGGCCGTT      180
147      ATCCATCTGG AGGCTGCAGG GTCCTTGGGG TAACAGGGAC CAC                                     223
149 (2) INFORMATION FOR SEQ ID NO: 9:
150      (i) SEQUENCE CHARACTERISTICS:
151      (A) LENGTH: 2393 base pairs

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152      (B) TYPE: nucleic acid
153      (C) STRANDEDNESS: single
154      (D) TOPOLOGY: linear
155      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
156      AAGGCCACCT CGCCGCTCTC CTGGATGCTG GCCTCGGCAG GCCCCCTGAA CCTGCTTCTT      60
157      TGGGCACTGT TGCTGAAACA GGCACAGATG GCCATGTACT TCTGGGAGAT GGGTTCCAAT      120
158      GCAGTTTCCT CAGCTCTTGG GGCCTGTTTG CTGCTCCGGG TGATGGCACG CCTGGAGCCT      180
159      GACGCTGAGG AGGCAGCACG GAGGAAAGAC CTGGCGTTCA AGTTTGAGGG GATGGGCGTT      240
160      GACCTCTTTG GCGAGTGCTA TCGCAGCAGT GAGGTGAGGG CTGCCCAGCT CCTCCTCCGT      300
161      CGYTGCCCGC TCTGGGGGGA TGCCACTTTG CCTTCCAGGT GGCCATGCAA AGCTGACGSC      360
162      CSTGMCTTCT TTGCCMAGGA TGGGGTACAG TCTCTGCTGA CACAGAAGTG GTGGGGAGAT      420
163      ATGGCCAGCA CTACACCCAT CTGGGCCCTG GTTATCGCGT TCTTTTGCCC TCCACTCATC      480
164      TACACCCGCC TCATCACCTT CAGGAAATCA GAAGAGGAGC CCACACGGGA GGAGCTAGAG      540
165      TTTGACATGG ATAGTGTAT TAATGGGGAA GGGCCTGTCT GGACGGCGGA CCCAGCCGAG      600
166      AAGACGCCGC TGGGGGTCCC GCGCCAGTCG GGCCGTCCGG GTTGCTGCGG GGGCCGCTGC      660
167      GGGGGGCGCC GGTGCCTACG CCGCTGGTTC CACTTCTGGG GCGCGCCGGT GACCATCTTC      720
168      ATGGGCAACG TGGTCAGCTA CCTGCTGTTC CTGCTGCTTT TCTCGCGGGT GCTGCTCGTG      780
169      GATTTCCAGC CGGCGCCGCC CGGCTCCCTG GAGCTGCTGC TCTATTTCTG GGCTTTACAG      840
170      CTGCTGTGCG AGGAATGCGC CAGGGCCTGA GCGGAGGCGG GGGCAGCCTC GCCAGCGGGG      900
171      GCCCCGGGCC TGGCCATGCC TCACTGAGCC AGCGCCTGCG CCTCTACCTC GCCGACAGCT      960
172      GGAACCAAGT CGACCTAGTG GCTCTCACCT GCTTCTCCTT GGGCGTGGGC TGCCGGCTGA      1020
173      CCCCAGGTTT GTACCACCTG GGCCGCACTG TCCTCTGCAT CGACTTCATG GTTTTCACGG      1080
174      TGCGGCTGCT TCACATCTTC ACGGTCAACA AACAGCTGGG GCCCAAGATC GTCATCGTGA      1140
175      GCAAGATGAT GAAGGACGTG TTCTTCTTCC TCTTCTTCCT CGGCGTGTGG CTGGTAGCCT      1200
176      ATGGCGTGGC CACGGAGGGG CTCCTGAGGC CACGGGACAG TGAATTCCCA AGTATCCTGC      1260
177      GCCGCGTCTT CTACCGTCCC TACCTGCAGA TCTTCGGGCA GATTCCCCAG GAGGACATGG      1320
178      ACGTGGCCCT CATGGAGCAC AGCAACTGCT GTCCGGAGCC CGGCTTCTGG GCACACCCTC      1380
179      CTGGGGCCCA GCGGGGCACC TGCGTCTCCC AGTATGCCAA CTGGCTGTGG GTGCTGCTCC      1440
180      TCGTCATCTT CCTGCTCGTG GCCAACATCC TGCTGGTCAA CTTGCTCATT GCCATGTTCA      1500
181      GTTACACATT CGGCAAAGTA CAGGGCAACA GCGATCTCTA CTGGAAGGCG CAGGTTACCG      1560
182      CCTCATCCGG GAATTCCACT CTCGGCCCGC GCTGGCCCCG CCCTTTATCG TCATCTCCCA      1620
183      CTTGCGCCTC CTGCTCAGGC AATTGTGCAG GCGACCCCGG AGCCCCCAGC CGTCTCCCC      1680
184      GGCCCTCGAG CATTTCCGGG TTTACCTTTC TAAGGAAGCC GAGCGGAAGC TGCTAACGTG      1740
185      GGAATCGGTG CATAAGGAGA ACTTTCTGCT GGCACGCGCT AGGGACAAGC GGGAGAGCGA      1800
186      CTCCGAGCGT CTGAAGCGCA CGTCCCAGAA GGTGGACTTG GCACTGAAAC AGCTGGGACA      1860
187      CATCCGCGAG TACGAACAGC GCCTGAAAGT GCTGGAGCGG GAGGTCCAGC AGTGTAGCCG      1920
188      CGTCTGGGGG TGGGTGGCCG AGGCCCTGAG CCGCTCTGCC TTGCTGCCCC CAGGTGGGCC      1980
189      GCCACCCCTT GACCTGCCTG GGTCCAAAGA CTGAGCCCTG CTGGCGGACT TCAAGGAGAA      2040
190      GCCCCACAG GGGATTTTGC TCCTAGAGTA AGGCTCATCT GGGCCTCGGC CCCCGCACCT      2100
191      GGTGGCCTTG TCCTTGAGGT GAGCCCCATG TCCATCTGGG CCACTGTGAG GACCACCTTT      2160
192      GGGAGTGTC TCCTTACAAA CCACAGCATG CCCGGTCTCT CCCAGAACCA GTCCCAGCCT      2220
193      GGGAGGATCA AGGCCTGGAT CCCGGGCCGT TATCCATCTG GAGGCTGCAG GGTCTTGGG      2280
194      GTAACAGGGA CCACAGACCC CTCACCACTC ACAGATTCTT CACACTGGGG AAATAAAGCC      2340
195      ATTTACAGAGG AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA GGGCGGCCGC GGT      2393
197      (2) INFORMATION FOR SEQ ID NO: 10:
198          (i) SEQUENCE CHARACTERISTICS:
199              (A) LENGTH: 1297 base pairs
200              (B) TYPE: nucleic acid
201              (C) STRANDEDNESS: single

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202         (D) TOPOLOGY: linear
203     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
204         GAATTCGGCT CGAGCAAACA GCTGGGGCCC AAGATCGTCA TCGTGAGCAA GATGATGAAG      60
205         GACGTGTTCT TCTTCTCTT CTTCTCGGC GTGTGGCTGG TAGCCTATGG CGTGGCCACG      120
206         GAGGGGCTCC TGAGGCCACG GGACAGTGAC TTCCCAAGTA TCCTGCGCCG CGTCTTCTAC      180
207         CGTCCCTACC TGCAGATCTT CGGGCAGATT CCCCAGGAGG ACATGGACGT GGCCCTCATG      240
208         GAGCACAGCA ACTGCTCGTC GGAGCCCGGC TTCTGGGCAC ACCCTCCTGG GGCCAGGCG      300
209         GGCACCTGCG TCTCCAGTA TGCCAAGTGG CTGGTGGTGC TGCTCCTCGT CATCTTCCTG      360
210         CTCGTGGCCA ACATCCTGCT GGTCAACTTG CTCATTGCCA TGTTCAAGTTA CACATTCGGC      420
211         AAAGTACAGG GCAACAGCGA TCTCTACTGG AAGGCGCAGC GTTACCGCCT CATCCGGGAA      480
212         TTCCACTCTC GGCCCGCGCT GGCCCGCCC TTTATCGTCA TCTCCACTT GCGCCTCCTG      540
213         CTCAGGCAAT TGTGCAGGCG ACCCGGAGC CCCCAGCCGT CCTCCCGGC CCTCGAGCAT      600
214         TTCCGGGTTT ACCTTTCTAA GGAAGCCGAG CGGAAGCTGC TAACGTGGGA ATCGGTGCAT      660
215         AAGGAGAACT TTCTGCTGGC ACGCGCTAGG GACAAGCGGG AGAGCGACTC CGAGCGTCTG      720
216         AAGCGCACGT CCCAGAAGT GGACTTGGCA CTGAAACAGC TGGGACACAT CCGCGAGTAC      780
217         GAACAGCGCC TGAAAGTGCT GGAGCGGGAG GTCCAGCAGT GTAGCCGCGT CCTGGGGTGG      840
218         GTGGCCGAGG CCCTGAGCCG CTCTGCCTTG CTGCCCCCAG GTGGGCCGCC ACCCCCTGAC      900
219         CTGCCTGGGT CCAAAGACTG AGCCCTGCTG GCGGACTTCA AGGAGAAGCC CCCACAGGGG      960
220         ATTTTGCTCC TAGAGTAAGG CTCATCTGGG CCTCGGCCCC CGCACCTGGT GGCCTTGTC      1020
221         TTGAGGTGAG CCCCATGTCC ATCTGGGCCA CTGTCAGGAC CACCTTTGGG AGTGTCTATCC      1080
222         TTACAAACCA CAGCATGCCC GGCTCCTCCC AGAACCAGTC CCAGCCTGGG AGGATCAAGG      1140
223         CCTGGATCCC GGGCCGTTAT CCATCTGGAG GCTGCAGGGT CCTTGGGGTA ACAGGGACCA      1200
224         CAGACCCCTC ACCACTCACA GATTCTCAC ACTGGGAAA TAAAGCCATT TCAGAGGAAA      1260
225         AAAAAAAAAA AAAAAAAAAA AAAAAAGGG CGGCCG      1297
227 (2) INFORMATION FOR SEQ ID NO: 11:
228     (i) SEQUENCE CHARACTERISTICS:
229         (A) LENGTH: 68 base pairs
230         (B) TYPE: nucleic acid
231         (C) STRANDEDNESS: single
232         (D) TOPOLOGY: linear
233     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
234         AGCTCGGAAT TCCGAGCTTG GATCCTCTAG AGCGGCCGCC GACTAGTGAG CTCGTCGACC      60
235         CGGGAATT      68
237 (2) INFORMATION FOR SEQ ID NO: 12:
238     (i) SEQUENCE CHARACTERISTICS:
239         (A) LENGTH: 68 base pairs
240         (B) TYPE: nucleic acid
241         (C) STRANDEDNESS: single
242         (D) TOPOLOGY: linear
243     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
244         AATTAATTC CGGTCGACG AGCTCACTAG TCGGCGGCCG CTCTAGAGGA TCCAAGCTCG      60
245         GAATTCG      68
247 (2) INFORMATION FOR SEQ ID NO: 13:
248     (i) SEQUENCE CHARACTERISTICS:
249         (A) LENGTH: 24 base pairs
250         (B) TYPE: nucleic acid
251         (C) STRANDEDNESS: single
252         (D) TOPOLOGY: linear
253     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

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RAW SEQUENCE LISTING ERROR SUMMARY

DATE: 02/10/2004

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Input Set : N:\Crf3\RULE60\10763992.RAW.txt

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Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 53,54,55,56,57,58,59
Seq#:2; Line(s) 68,69,70,71
Seq#:3; Line(s) 80,81,82,83
Seq#:4; Line(s) 92,93,94,95,96
Seq#:5; Line(s) 105,106,107,108,109
Seq#:6; Line(s) 118,119,120,121,122
Seq#:7; Line(s) 131,132,133,134,135
Seq#:8; Line(s) 144,145,146,147
Seq#:9; Line(s) 156,157,158,159,160,161,162,163,164,165,166,167,168,169,170
Seq#:9; Line(s) 171,172,173,174,175,176,177,178,179,180,181,182,183,184,185
Seq#:9; Line(s) 186,187,188,189,190,191,192,193,194,195
Seq#:10; Line(s) 204,205,206,207,208,209,210,211,212,213,214,215,216,217
Seq#:10; Line(s) 218,219,220,221,222,223,224,225
Seq#:11; Line(s) 234,235
Seq#:12; Line(s) 244,245
Seq#:13; Line(s) 254
Seq#:14; Line(s) 263
Seq#:15; Line(s) 272
Seq#:16; Line(s) 281
Seq#:17; Line(s) 290
Seq#:18; Line(s) 299
Seq#:19; Line(s) 308
Seq#:20; Line(s) 317
Seq#:21; Line(s) 326
Seq#:22; Line(s) 335
Seq#:23; Line(s) 344
Seq#:24; Line(s) 353

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/763,992

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Input Set : N:\Crf3\RULE60\10763992.RAW.txt

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L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:361 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=25
L:454 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=26
L:466 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=27
L:477 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=28
L:488 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=29
L:499 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=30
L:510 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=31
L:521 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=32
L:532 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=33